In the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A polypeptide ~~Polypeptide~~, which has a binding affinity for HER2 and which is related to a domain of staphylococcal protein A (SPA) in that the sequence of the polypeptide corresponds to the sequence of the SPA domain having from 1 to about 20 substitution mutations.

2. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 1, which has a binding affinity for HER2 such that the K_D value of the interaction is at most 1×10^{-6} M.

3. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 2, which has a binding affinity for HER2 such that the K_D value of the interaction is at most 1×10^{-7} M.

4. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 1 ~~any one of claims 1-3~~, the sequence of which corresponds to the sequence of SPA protein Z, as set forth in SEQ ID NO:1, comprising from 1 to about 2 substitution mutations.

5. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4, comprising from 4 to about 20 substitution mutations.

6. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~or 5~~, comprising substitution mutations at one or more of the positions 13, 14, 28, 32 and 35.

7. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 6, additionally comprising substitution mutations at one or more of the positions 9, 10, 11, 17, 18, 24, 25 and 27.

8. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-7~~, comprising a substitution mutation at position 13 from phenylalanine to tyrosine.

9. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-8~~, comprising a substitution mutation at position 14 from tyrosine to tryptophan.

10. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims~~ 4-9, comprising a substitution mutation at position 28 from asparagine to an amino acid residue selected from arginine and histidine.

11. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-10~~, comprising a substitution mutation at position 28 from asparagine to arginine.

12. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-11~~, comprising a substitution mutation at position 32 from glutamine to arginine.

13. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-12~~, comprising a substitution mutation at position 35 from lysine to tyrosine.

14. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-13~~, comprising a substitution mutation at position 10 from glutamine to arginine.

15. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-14~~, comprising a substitution mutation at position 11 from asparagine to threonine.

16. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-15~~, comprising a substitution mutation at position 17 from leucine to valine.

17. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-12~~, comprising a substitution mutation at position 27 from arginine to an amino acid residue selected from lysine and serine.

18. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-17~~, the amino acid sequence of which corresponds to that of SEQ ID NO:1, comprising at least the following mutations: F13Y, Y14W, N28R, Q32R and K35Y.

19. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 4 ~~any one of claims 4-18~~, the amino acid sequence of which is as set out in any one of SEQ ID NO:2-79.

20. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 19, the amino acid sequence of which is as set out in any one of SEQ ID NO:2-3.

21. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 1 ~~any preceding claim~~, in which at least one of the asparagine residues present in the domain of staphylococcal protein A (SPA) to which said polypeptide is related has been replaced with another amino acid residue.

22. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 21, the sequence of said domain of staphylococcal protein A (SPA) corresponding to the sequence of SPA protein Z as set forth in SEQ ID NO:1, and the polypeptide comprising substitution mutations at at least one position chosen from N3, N6, N11, N21, N23, N28, N43 and N52.

23. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 22, comprising at least one of the following mutations: N3A, N6A, N6D, N11S, N23T, N28A and N43E.

24. (Currently Amended) A polypeptide ~~Polypeptide~~, which constitutes a fragment of a polypeptide according to claim 1 ~~any preceding claim~~, which fragment retains binding affinity for HER2.

25. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 1 ~~any preceding claim~~, which comprises additional amino acid residues at either terminal.

26. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 25, in which the additional amino acid residues

comprise a cysteine residue at the N- or C-terminal of the polypeptide.

27. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 25 ~~any one of claims 25-26~~, in which the additional amino acid residues comprise a tag, preferably chosen from a hexahistidinyl tag, a myc tag and a flag tag.

28. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 25 ~~any one of claims 25-26~~, in which the additional amino acid residues comprise at least one functional polypeptide domain, so that the polypeptide is a fusion polypeptide between a first moiety, consisting of the polypeptide according to claim 1 ~~any one of claims 1-24~~, and at least one second and optionally further moiety or moieties.

29. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 28, in which the second moiety consists of one or more polypeptide(s) according to claim 1 ~~any one of claims 1-24~~, making the polypeptide a multimer of HER2 binding polypeptides according to claim 1 ~~any of claims 1-24~~, the sequences of which may be the same or different.

30. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 28, in which the second moiety comprises at least one polypeptide domain capable of binding to a target molecule other than HER2.

31. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 30, in which the second moiety comprises at least one

polypeptide domain capable of binding to human serum albumin.

32. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 31, in which the at least one polypeptide domain capable of binding to human serum albumin is the albumin binding domain of streptococcal protein G.

33. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 30, in which the second moiety comprises a polypeptide which is related to a domain of staphylococcal protein A (SPA) in that the sequence of the polypeptide corresponds to the sequence of the SPA domain having from 1 to about 20 substitution mutations.

34. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 33, in which the sequence of the second moiety polypeptide corresponds to the sequence of SPA protein Z, as set forth in SEQ ID NO:1, having from 1 to about 20 substitution mutations.

35. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 28, in which the second moiety is capable of enzymatic action.

36. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 28, in which the second moiety is capable of fluorescent action.

37. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 28, in which the second moiety is a phage coat protein or a fragment thereof.

38. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 1 ~~any preceding claim~~, which comprises a label group.

39. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 38, in which the label group is chosen from fluorescent labels, biotin and radioactive labels.

40. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 1 ~~any one of the preceding claims~~, coupled to a substance having an activity against cells overexpressing HER2.

41. (Currently Amended) A polypeptide ~~Polypeptide~~ according to claim 40, in which said substance having an activity against cells overexpressing HER2 is chosen from cytotoxic agents, radioactive agents, enzymes for ADEPT applications, cytokines and procoagulant factors.

42. (Currently Amended) A nucleic ~~Nucleic~~ acid molecule comprising a sequence encoding a polypeptide according to claim 1 ~~any one of claims 1 to 37~~.

43. (Currently Amended) An expresson ~~Expression~~ vector comprising the nucleic acid molecule according to claim 42.

44. (Currently Amended) A host ~~Host~~ cell comprising the expression vector according to claim 43.

45. (Canceled)

46. (Canceled)

47. (Currently Amended) A method ~~Method~~ of treatment of at least one form of cancer characterized by over-expression of HER2, which method comprises administering to a subject in need of such treatment a therapeutically effective amount of a composition, which comprises a polypeptide according to claim 1 ~~any one of claims 1-41~~ as an active substance.

48. (Canceled)

49. (Currently Amended) A method ~~Method~~ of directing a substance having an anti-cancer activity to cells overexpressing HER2 *in vivo*, which method comprises administering a conjugate of said substance and a polypeptide according to claim 1 ~~any one of claims 1-41~~ to a subject.

50. (Canceled)

51. (Currently Amended) A method ~~Method~~ of detection of HER2 in a sample, in which method a polypeptide according to claim 1 ~~any one of claims 1-41~~ is used.

52. (Currently Amended) A method ~~Method~~ according to claim 51, comprising the steps: (i) providing a sample to be tested, (ii) applying a polypeptide according to claim 1 ~~any one of claims 1-41~~ to the sample under conditions such that binding of the polypeptide to any HER2 present in the sample is enabled, (iii) removing non-bound polypeptide, and (iv) detecting bound polypeptide.

53. (Currently Amended) A method ~~Method~~ according to claim 52, in which the sample is a biological fluid sample, preferably a human blood plasma sample.

54. (Currently Amended) A method ~~Method~~ according to claim 52, in which the sample is a tissue sample, preferably a human tissue sample, more preferably a biopsy sample from a human suffering from cancer.

55. (Currently Amended) A kit ~~Kit~~ for diagnosis of HER2 overexpression in a tissue sample, which kit comprises a polypeptide according to claim 1 ~~any one of claims 1-41~~ fused to a reporter enzyme, reagents for detection of activity of said reporter enzyme, and positive and negative control tissues slides.

56. (Currently Amended) A kit ~~Kit~~ for *in vivo* diagnosis of HER2 overexpression, which kit comprises a polypeptide according to claim 1 ~~any one of claims 1-41~~ labeled with a chelator, a diagnostic radioactive isotope, and reagents for the analysis of the incorporation efficiency.

57. (Currently Amended) A kit ~~Kit~~ for performing the method of claim 49, which kit comprises a polypeptide according to claim 1 ~~any one of claims 1-41~~ labeled with a chelator, a therapeutic radioactive isotope, and reagents for the analysis of the incorporation efficiency.